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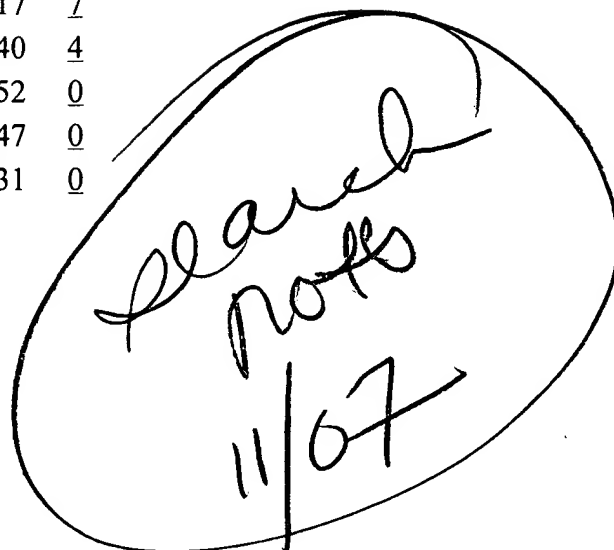
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Term	Documents
((1.TI,AB,CLM.) AND 4).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	31
(L4 AND L1.TI,AB,CLM.).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	31

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<u>#30</u> Search urea amidohydrolase helicobacter felis	17:30:37	<u>39</u>
<u>#27</u> Search several helicobacter ureases	17:22:35	<u>28</u>
<u>#26</u> Search several ureases	17:22:15	<u>118</u>
<u>#25</u> Search isoforms ureases	17:21:17	<u>7</u>
<u>#24</u> Search multiple ureases	17:20:40	<u>4</u>
<u>#23</u> Search helicobacter felis urease subunit y	17:09:52	<u>0</u>
<u>#22</u> Search helicobacter felis urease subunit x	17:09:47	<u>0</u>
<u>#20</u> Search helicobacter felis urease xy	17:09:31	<u>0</u>
<u>#21</u> Search helicobacter felis urexy		



11/15/99
ALIGNED SEQUENCES

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Sequence 3:	1	-	226	(226 aa)	99%
Sequence 4:	1	-	226	(226 aa)	99%
Sequence 5:	1	-	226	(226 aa)	99%
Sequence 6:	1	-	237	(237 aa)	50%
Sequence 7:	1	-	238	(238 aa)	52%
Sequence 8:	1	-	234	(234 aa)	54%

Alignment type: Global Protein
Parameters: Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N

[illegible]

Figure 1b